



SEQUENCE LISTING

Cahoon, Rebecca E
Miao, Gou-Hau
Powell, Wayne

<120> Plant Farnesyltransferases

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<151> 1998-09-08

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<212> DNA

<213> Zea mays

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<212> PRT

<213> Zea mays

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097667-0001

00786675-030701

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<213> Oryza sativa

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Arg Glu Val Met Asp Tyr Phe Arg Ala Leu Tyr Phe Ala Gly Glu Arg
50 55 60
Ser Val Arg Ala Leu His Leu Thr Ala Glu Val Ile Asp Leu Asn Pro
65 70 75 80
Gly Asn Tyr Thr Val Trp His Phe Arg Arg Leu Val Leu Glu Ala Leu
85 90 95
Asp Ala Asp Leu Arg Glu Glu Met Asp Phe Val Asp Arg Ile Ala Glu
100 105 110
Cys Asn Pro Lys Asn Tyr Gln Ile Trp His His Lys Arg Trp Leu Ala
115 120 125
Glu Lys Leu Gly Pro Asp Ile Ala Asn Lys Glu His Glu Phe Thr Arg
130 135 140
Lys Ile Leu Ser Met Asp Ala Lys Asn Tyr His Ala Trp Ser His Arg
145 150 155 160

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 Cys Asn Gln Leu Leu Glu Glu Asp Val Phe Asn Asn Ser Ala Trp Asn
 180 185 190
 Gln Arg Tyr Leu Val Ile Thr Ser Ser Pro Leu Leu Gly Gly Leu Ala
 195 200 205
 Ala Met Arg Asp Ser Glu Val Asp Tyr Thr Val Gly Ala Ile Leu Ala
 210 215 220
 Asn Pro Gln Asn Glu Ser Pro Trp Arg Tyr Leu Lys Gly Leu Tyr Lys
 225 230 235 240
 Gly Glu Asn Asn Leu Leu Met Ala Asp Glu Arg Ile Ser Asp Val Cys
 245 250 255
 Leu Lys Val Leu Lys His Asp Ser Thr Cys Val Phe Ala Leu Ser Leu
 260 265 270
 Leu Leu Asp Leu Leu Gln Ile Gly Leu Gln Pro Ser Asp Glu Leu Lys
 275 280 285
 Gly Thr Ile Glu Ala Ile Lys Asn Ser Asp Pro Glu Ala Asp Glu Ala
 290 295 300
 Val Asp Ala Asp Leu Ala Thr Ala Ile Cys Ser Ile Leu Gln Arg Cys
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 Ser Gln Thr

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 a 1261

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 35 40 45
 Glu Val Met Asp Tyr Phe Arg Ala Val Tyr Leu Thr Asp Glu Arg Ser
 50 55 60
 Pro Arg Ala Leu Ala Leu Thr Ala Glu Ala Val Gln Phe Asn Ser Gly
 65 70 75 80
 Asn Tyr Thr Val Trp His Phe Arg Arg Leu Leu Leu Glu Ser Leu Lys
 85 90 95
 Val Asp Leu Asn Asp Glu Leu Asp Phe Val Glu Arg Met Ala Ala Gly
 100 105 110
 Asn Ser Lys Asn Tyr Gln Met Trp His His Arg Arg Trp Val Ala Glu
 115 120 125
 Lys Leu Gly Pro Glu Ala Arg Asn Asn Glu Leu Glu Phe Thr Lys Lys
 130 135 140
 Ile Leu Ser Val Asp Ala Lys His Tyr His Ala Trp Ser His Arg Gln
 145 150 155 160
 Trp Ala Leu Gln Thr Leu Gly Gly Trp Glu Asp Glu Leu Asn Tyr Cys
 165 170 175
 Thr Glu Leu Leu Lys Glu Asp Ile Phe Asn Asn Ser Ala Trp Asn Gln
 180 185 190
 Arg Tyr Phe Val Ile Thr Arg Ser Pro Phe Leu Gly Gly Leu Lys Ala
 195 200 205
 Met Arg Glu Ser Glu Val Leu Tyr Thr Ile Glu Ala Ile Ile Ala Tyr
 210 215 220
 Pro Glu Asn Glu Ser Ser Trp Arg Tyr Leu Arg Gly Leu Tyr Lys Gly
 225 230 235 240
 Glu Thr Thr Ser Trp Val Asn Asp Pro Gln Val Ser Ser Val Cys Leu
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 Lys Ile Leu Arg Thr Lys Ser Asn Tyr Val Phe Ala Leu Ser Thr Ile
 260 265 270

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 Pro Arg Ala Leu Ala Leu Thr Ala Glu Ala Val Gln Phe Asn Ser Gly
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 85 90 95
 Val Asp Leu Asn Asp Glu Leu Glu Phe Val Glu Arg Met Ala Ala Gly
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 Asn Ser Lys Asn Tyr Gln Met Trp Cys Asp Ala Leu Leu Cys Ser Phe
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 Phe His Thr Leu His His Arg Arg Trp Val Ala Glu Lys Leu Gly Pro
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 145 150 155 160
 Asp Ala Lys His Tyr His Ala Trp Ser His Arg Gln Trp Ala Leu Gln
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 180 185 190
 Lys Glu Asp Ile Phe Asn Asn Ser Ala Trp Asn Gln Arg Tyr Phe Val
 195 200 205
 Ile Thr Arg Ser Pro Phe Leu Gly Gly Leu Lys Ala Met Arg Glu Ser
 210 215 220
 Glu Val Leu Tyr Thr Ile Glu Ala Ile Ile Ala Tyr Pro Glu Asn Glu
 225 230 235 240
 Ser Ser Trp Arg Tyr Leu Arg Gly Leu Tyr Lys Gly Glu Thr Thr Ser
 245 250 255
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 Thr Lys Ser Asn Tyr Val Phe Ala Leu Ser Thr Ile Leu Asp Leu Ile
 275 280 285
 Cys Phe Gly Tyr Gln Pro Asn Glu Asp Ile Arg Asp Ala Ile Asp Ala
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 Gly Glu Gln Gln Asn Leu Asn Ile Ala Arg Asn Ile Cys Ser Ile Leu
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 35 40 45
 Asp Ala Ile His Leu Asn Pro Gly Asn Tyr Thr Val Trp His Phe Arg
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 Arg Val Val Leu Glu Ala Leu Asp Ala Asp Leu Leu Leu Glu Met His
 65 70 75 80
 Phe Val Asp Gln Ile Ala Glu Ser Asn Pro Lys Asn Tyr Gln Val Trp
 85 90 95
 His His Lys Arg Trp Leu Ala Glu Lys Ile Gly Pro Asp Ala Ala Asn
 100 105 110
 Ser Glu His Asp Phe Thr Arg Lys Ile Leu Ala Met Asp Ala Lys Asn
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Phe	His	Val	Leu	Asp	Ala	Asn	Arg	Pro	Trp	Leu	Cys	Tyr	Trp	Met	Val
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Tyr	Thr	Ala	Ile	Ser	Val	Ala	Ser	Leu	Val	Asn	Ile	Leu	Asp	Phe	Lys
		195					200					205			
Leu	Ala	Lys	Gly	Val	Gly	Asp	Tyr	Ile	Ala	Arg	Cys	Gln	Thr	Tyr	Glu
	210					215					220				
Gly	Gly	Ile	Ala	Gly	Glu	Pro	Tyr	Ala	Glu	Ala	His	Gly	Gly	Tyr	Thr
	225				230					235					240
Phe	Cys	Gly	Leu	Ala	Ala	Leu	Ile	Leu	Leu	Asn	Glu	Ala	Glu	Lys	Val
			245						250					255	
Asp	Leu	Pro	Ser	Leu	Ile	Gly	Trp	Val	Ala	Phe	Arg	Gln	Gly	Val	Glu
			260					265					270		
Cys	Gly	Phe	Gln	Gly	Arg	Thr	Asn	Lys	Leu	Val	Asp	Gly	Cys	Tyr	Ser

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275

280

285

Phe Trp Gln Gly Ala Ala Ile Ala Phe Thr Gln Lys Leu Ile Thr Ile
290 295 300

Val Asp Lys Gln Leu Lys Ser Ser Tyr Ser Cys Lys Arg Pro Ser Gly
305 310 315 320

Glu Asp Ala Cys Ser Thr Ser Ser Tyr Gly Cys Thr Ala Lys Lys Ser
325 330 335

Ser Ser Ala Val Asp Tyr Ala Lys Phe Gly Phe Asp Phe Ile Gln Gln
340 345 350

Ser Asn Gln Ile Gly Pro Leu Phe His Asn Ile Ala Leu Gln Gln Tyr
355 360 365

Ile Leu Leu Cys Ser Gln Val Leu Glu Gly Gly Leu Arg Asp Lys Pro
370 375 380

Gly Lys Asn Arg Asp His Tyr His Ser Cys Tyr Cys Leu Ser Gly Leu
385 390 395 400

Ala Val Ser Gln Tyr Ser Ala Met Thr Asp Thr Gly Ser Cys Pro Leu
405 410 415

Pro Gln His Val Leu Gly Pro Tyr Ser Asn Leu Leu Glu Pro Ile His
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Pro Leu Tyr Asn Val Val Leu Asp Lys Tyr His Thr Ala Tyr Glu Phe
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Phe Ser Glu Glu
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<210> 13

<211> 1031

<212> DNA

<213> Oryza sativa

<400> 13

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ccatatactc ctgctgctgc tgagggcggt ccggcagcgg atagccaggc cgctgagctg 180
ccccggctga ctgtgacgca ggtggagcag atgaagggtg aggcgaaggt gggcgaaatc 240
taccgcgtcc tcttcggcaa cgcgcccaac gccaatcccc tcatgttaga gctgtggcgt 300
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gatggtggtt atggcggagg acctggacag ttgcctcatc tcgctacaac ttatgctgct 540
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cttgatggtg aactagcaaa aggtgttgga aattacataa caaggtgtca aacctatgaa 780
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gctacgatga tctgtcttaa cgaagtggac aaacttgatt tggctagctt gattggctgg 900
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<210> 14

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<211> 313
 <212> PRT
 <213> Oryza sativa

<400> 14

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			20					25					30				
Leu	Thr	Val	Thr	Gln	Val	Glu	Gln	Met	Lys	Val	Glu	Ala	Lys	Val	Gly		
		35					40					45					
Glu	Ile	Tyr	Arg	Val	Leu	Phe	Gly	Asn	Ala	Pro	Asn	Ala	Asn	Ser	Leu		
	50					55					60						
Met	Leu	Glu	Leu	Trp	Arg	Glu	Gln	His	Val	Glu	Tyr	Leu	Thr	Arg	Gly		
	65				70					75					80		
Leu	Lys	His	Leu	Gly	Pro	Ser	Phe	His	Val	Leu	Asp	Ala	Asn	Arg	Pro		
				85					90					95			
Trp	Leu	Cys	Tyr	Trp	Ile	Ile	His	Ala	Leu	Ala	Leu	Leu	Asp	Glu	Ile		
			100					105						110			
Pro	Asp	Asp	Val	Glu	Asp	Asp	Ile	Val	Asp	Phe	Leu	Ser	Arg	Cys	Gln		
		115					120					125					
Asp	Lys	Asp	Gly	Gly	Tyr	Gly	Gly	Gly	Pro	Gly	Gln	Leu	Pro	His	Leu		
	130					135					140						
Ala	Thr	Thr	Tyr	Ala	Ala	Val	Asn	Thr	Leu	Val	Thr	Ile	Gly	Ser	Glu		
	145				150					155					160		
Arg	Ala	Leu	Ser	Ser	Val	Asn	Arg	Asp	Asn	Leu	Tyr	Lys	Phe	Met	Leu		
			165					170						175			
Arg	Met	Lys	Asp	Thr	Ser	Gly	Ala	Phe	Arg	Met	His	Asp	Gly	Gly	Glu		
		180						185					190				
Ile	Asp	Val	Arg	Ala	Ser	Tyr	Thr	Ala	Ile	Ser	Val	Ala	Ser	Leu	Val		
	195						200					205					
Asn	Ile	Leu	Asp	Gly	Glu	Leu	Ala	Lys	Gly	Val	Gly	Asn	Tyr	Ile	Thr		
	210					215					220						
Arg	Cys	Gln	Thr	Tyr	Glu	Gly	Gly	Ile	Ala	Gly	Glu	Pro	Tyr	Ala	Glu		
	225				230					235					240		
Ala	His	Gly	Gly	Tyr	Thr	Phe	Cys	Gly	Leu	Ala	Thr	Met	Ile	Leu	Leu		
			245						250					255			
Asn	Glu	Val	Asp	Lys	Leu	Asp	Leu	Ala	Ser	Leu	Ile	Gly	Trp	Val	Ala		
		260					265						270				
Phe	Arg	Gln	Gly	Val	Glu	Cys	Gly	Phe	Gln	Gly	Arg	Thr	Asn	Lys	Leu		
		275					280					285					
Val	Asp	Gly	Cys	Tyr	Ser	Phe	Trp	Gln	Gly	Ala	Ala	Leu	Ala	Leu	Thr		
	290					295					300						

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Val His Arg Val Ala Pro Thr Ala Lys
305 310

<210> 15
<211> 1504
<212> DNA
<213> Glycine max

<400> 15
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cccaaaccct catgttggag cttcaacgcg ataatacat gcagtatgtc tccaaaggcc 180
ttcgccatct cagttccgca ttttccgttt tggacgctaa tcgaccctgg ctctgctact 240
ggatcttcca ctccattgct ttgtcgggag aatccgtcga tgatgaactc gaagataacg 300
ctatcgattt tcttaaccgt tgccaggatc cgaatgggtg atatgccggg ggaccaggcc 360
agatgcctca tattgccaca acttatgctg ctgttaattc acttattact ttgggtggtg 420
agaaatccct ggcatacaatt aatagagata aactgtatgg gtttctgcgg cggatgaagc 480
aaccaaatgg tggattcagg atgcatgatg aagggtgaaat tgatgttcga gcttgctaca 540
ctgccatttc tgttgcaagt gttttgaaca ttttggatga tgagctgatc cagaatgttg 600
gagactacat tataagctgt caaacatatg aggggtggcat tgctgggtgag cctgggttctg 660
aggctcatgg tgggtacacc ttttgtggat tagctacaat gattctgatt ggtgagggtta 720
atcattgga tctgcctcga ttagttgact ggggtggtatt ccgacaagggt aaggaatgtg 780
gattccaggg gagaacaaat aaactgggtg atggatgcta ttccttttgg caggggaggtg 840
ctgttgctct attgcaaaga ttatcttcta ttatcaacaa acagatggaa gagacatcac 900
agatttttgc ggtatcttat gtatctgaag caaaagaaag tttggatgga acctctagtc 960
atgcaacatg ccgtgggtgag catgaaggca ccagtgaatc cagttcatct gattttaaaa 1020
atattgccta taaattttatt aatgagtggg gagcacaaga accacttttt cacagtattg 1080
ctttacagca atatattctc ttatgtgcac aggagcaaga ggggtggactg agagacaaac 1140
cgggtaaacg tagagatcat tatcacacat gttactgttt aagtggactc tcattgtgcc 1200
agtatagttg gtcaaagcac ccagattctc caccactgcc taatctagta ttaggcccct 1260
actctaactc cttagaacca atccaccccc tctttaatgt tgtcttggga cgatatcgtg 1320
aagctcatga attcttcttt actgagtcgt gaccactggg tttagctacc aacaacttta 1380
tttgataaat gtaaaataaa ttcattggaa catataaatg taaaacagca ttggattaaa 1440
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaaa 1504

<210> 16
<211> 429
<212> PRT
<213> Glycine max

<400> 16
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Pro Arg Asn Ala Gln Thr Leu Met Leu Glu Leu Gln Arg Asp Asn His
20 25 30
Met Gln Tyr Val Ser Lys Gly Leu Arg His Leu Ser Ser Ala Phe Ser
35 40 45
Val Leu Asp Ala Asn Arg Pro Trp Leu Cys Tyr Trp Ile Phe His Ser
50 55 60
Ile Ala Leu Ser Gly Glu Ser Val Asp Asp Glu Leu Glu Asp Asn Ala
65 70 75 80
Ile Asp Phe Leu Asn Arg Cys Gln Asp Pro Asn Gly Gly Tyr Ala Gly
85 90 95

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Gly	Pro	Gly	Gln	Met	Pro	His	Ile	Ala	Thr	Thr	Tyr	Ala	Ala	Val	Asn		
			100					105						110			
Ser	Leu	Ile	Thr	Leu	Gly	Gly	Glu	Lys	Ser	Leu	Ala	Ser	Ile	Asn	Arg		
		115					120						125				
Asp	Lys	Leu	Tyr	Gly	Phe	Leu	Arg	Arg	Met	Lys	Gln	Pro	Asn	Gly	Gly		
	130					135					140						
Phe	Arg	Met	His	Asp	Glu	Gly	Glu	Ile	Asp	Val	Arg	Ala	Cys	Tyr	Thr		
145					150					155					160		
Ala	Ile	Ser	Val	Ala	Ser	Val	Leu	Asn	Ile	Leu	Asp	Asp	Glu	Leu	Ile		
				165					170						175		
Gln	Asn	Val	Gly	Asp	Tyr	Ile	Ile	Ser	Cys	Gln	Thr	Tyr	Glu	Gly	Gly		
			180					185						190			
Ile	Ala	Gly	Glu	Pro	Gly	Ser	Glu	Ala	His	Gly	Gly	Tyr	Thr	Phe	Cys		
		195					200					205					
Gly	Leu	Ala	Thr	Met	Ile	Leu	Ile	Gly	Glu	Val	Asn	His	Leu	Asp	Leu		
	210					215					220						
Pro	Arg	Leu	Val	Asp	Trp	Val	Val	Phe	Arg	Gln	Gly	Lys	Glu	Cys	Gly		
225					230					235					240		
Phe	Gln	Gly	Arg	Thr	Asn	Lys	Leu	Val	Asp	Gly	Cys	Tyr	Ser	Phe	Trp		
				245					250					255			
Gln	Gly	Gly	Ala	Val	Ala	Leu	Leu	Gln	Arg	Leu	Ser	Ser	Ile	Ile	Asn		
			260					265						270			
Lys	Gln	Met	Glu	Glu	Thr	Ser	Gln	Ile	Phe	Ala	Val	Ser	Tyr	Val	Ser		
		275					280						285				
Glu	Ala	Lys	Glu	Ser	Leu	Asp	Gly	Thr	Ser	Ser	His	Ala	Thr	Cys	Arg		
	290					295					300						
Gly	Glu	His	Glu	Gly	Thr	Ser	Glu	Ser	Ser	Ser	Ser	Asp	Phe	Lys	Asn		
305					310						315				320		
Ile	Ala	Tyr	Lys	Phe	Ile	Asn	Glu	Trp	Arg	Ala	Gln	Glu	Pro	Leu	Phe		
				325					330					335			
His	Ser	Ile	Ala	Leu	Gln	Gln	Tyr	Ile	Leu	Leu	Cys	Ala	Gln	Glu	Gln		
			340					345					350				
Glu	Gly	Gly	Leu	Arg	Asp	Lys	Pro	Gly	Lys	Arg	Arg	Asp	His	Tyr	His		
		355					360					365					
Thr	Cys	Tyr	Cys	Leu	Ser	Gly	Leu	Ser	Leu	Cys	Gln	Tyr	Ser	Trp	Ser		
	370					375						380					
Lys	His	Pro	Asp	Ser	Pro	Pro	Leu	Pro	Asn	Leu	Val	Leu	Gly	Pro	Tyr		
385					390					395				400			
Ser	Asn	Leu	Leu	Glu	Pro	Ile	His	Pro	Leu	Phe	Asn	Val	Val	Leu	Gly		
				405					410					415			
Arg	Tyr	Arg	Glu	Ala	His	Glu	Phe	Phe	Phe	Thr	Glu	Ser					

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<210> 17
 <211> 533
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (499)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (525)
 <223> n = A, C, G or T

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 gcccaaaacc tcatgttaga gctgcaacgc gataatcaca tgcagtatct ctccaaaggc 180
 ctacgccatc tcagttccgc gttttctgtc ttggacgcta atcgaccctg gctctgttac 240
 tggatcttcc attccattgc ttgtctggga gaatccgtcg acgacgaact cgaagataac 300
 actatcgatt ttcttaaccg ttgccaggat ccgaatggtg gatatgctgg gggaccaggc 360
 cagatgcctc acattgccac aacatatgct gcagttaata cacttattac tttgggtggt 420
 cagaaatcct ggcattcaatt aatagggtgag ataaactgta tgggtttctg cggcggatga 480
 agcaatcaaa tgggggggant caagatgcat gatgaaagga gaaanttgat gtc 533

<210> 18
 <211> 141
 <212> PRT
 <213> Glycine max

<400> 18
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 Asp Gln Trp Met Val Glu Ser Gln Val Phe Gln Ile Tyr Gln Leu Phe
 20 25 30
 Ala Thr Ile Pro Gly Ser Ala Gln Asn Leu Met Leu Glu Leu Gln Arg
 35 40 45
 Asp Asn His Met Gln Tyr Leu Ser Lys Gly Leu Arg His Leu Ser Ser
 50 55 60
 Ala Phe Ser Val Leu Asp Ala Asn Arg Pro Trp Leu Cys Tyr Trp Ile
 65 70 75 80
 Phe His Ser Ile Ala Leu Leu Gly Glu Ser Val Asp Asp Glu Leu Glu
 85 90 95
 Asp Asn Thr Ile Asp Phe Leu Asn Arg Cys Gln Asp Pro Asn Gly Gly
 100 105 110
 Tyr Ala Gly Gly Pro Gly Gln Met Pro His Ile Ala Thr Thr Tyr Ala
 115 120 125
 Ala Val Asn Thr Leu Ile Thr Leu Gly Gly Gln Lys Ser
 130 135 140

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<210> 19
 <211> 333
 <212> PRT
 <213> Pisum sativum

<400> 19

Met	Ala	Gly	Asn	Ile	Glu	Val	Glu	Glu	Asp	Asp	Arg	Val	Pro	Leu	Arg
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Leu	Arg	Pro	Glu	Trp	Ser	Asp	Val	Thr	Pro	Ile	Pro	Gln	Asp	Asp	Gly
			20					25					30		
Pro	Ser	Pro	Val	Val	Pro	Ile	Asn	Tyr	Ser	Glu	Glu	Phe	Ser	Glu	Val
		35					40					45			
Met	Asp	Tyr	Phe	Arg	Ala	Val	Tyr	Phe	Ala	Lys	Glu	Leu	Ser	Ser	Arg
	50					55					60				
Ala	Leu	Ala	Leu	Thr	Ala	Glu	Ala	Ile	Gly	Leu	Asn	Ala	Gly	Asn	Tyr
65					70					75					80
Thr	Val	Trp	His	Phe	Arg	Arg	Leu	Leu	Leu	Glu	Ser	Leu	Lys	Val	Asp
				85					90					95	
Leu	His	Val	Glu	Arg	Glu	Phe	Val	Glu	Arg	Val	Ala	Ser	Gly	Asn	Ser
			100					105						110	
Lys	Asn	Tyr	Gln	Ile	Trp	His	His	Arg	Arg	Trp	Val	Ala	Glu	Lys	Leu
		115					120					125			
Gly	Pro	Glu	Ala	Arg	Asn	Ser	Glu	Leu	Glu	Phe	Thr	Lys	Lys	Ile	Leu
	130					135					140				
Ser	Val	Asp	Ala	Lys	His	Tyr	His	Ala	Trp	Ser	His	Arg	Gln	Trp	Val
145					150					155					160
Leu	Gln	Asn	Leu	Gly	Gly	Trp	Glu	Asp	Glu	Leu	Ser	Tyr	Cys	Ser	Glu
			165						170					175	
Leu	Leu	Ala	Glu	Asp	Ile	Phe	Asn	Asn	Ser	Ala	Trp	Asn	Gln	Arg	Tyr
			180					185					190		
Phe	Val	Ile	Thr	Arg	Ser	Pro	Val	Leu	Gly	Gly	Leu	Lys	Ala	Met	Arg
		195					200					205			
Glu	Ser	Glu	Val	Leu	Phe	Thr	Val	Glu	Ala	Ile	Ile	Ser	Tyr	Pro	Glu
	210					215					220				
Asn	Glu	Ser	Ser	Trp	Arg	Tyr	Leu	Arg	Gly	Leu	Phe	Lys	Asp	Glu	Ser
225					230					235					240
Thr	Leu	Tyr	Val	Asn	Asp	Ala	Gln	Val	Ser	Ser	Leu	Cys	Leu	Lys	Ile
			245						250					255	
Leu	Lys	Thr	Lys	Ser	Asn	Tyr	Leu	Phe	Ala	Leu	Ser	Thr	Leu	Leu	Asp
			260					265					270		
Leu	Ser	Ala	Ser	Val	Ile	Gln	Pro	Asn	Glu	Asp	Phe	Arg	Asp	Ala	Ile
		275					280					285			
Glu	Ala	Leu	Arg	Leu	Gln	Ile	Leu	Ile	Lys	Gln	Asp	Ser	Asp	Ile	Ala

09365-0001

290

295

300

Ile Thr Ile Cys Ser Ile Leu Glu Gln Val Asp Pro Ile Arg Val Asn
305 310 315 320

Tyr Trp Val Trp Arg Lys Ser Arg Leu Pro Gln Ala Ala
325 330

<210> 20

<211> 326

<212> PRT

<213> Arabidopsis thaliana

<400> 20

Met Asn Phe Asp Glu Thr Val Pro Leu Ser Gln Arg Leu Glu Trp Ser
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Asp Val Val Pro Leu Thr Gln Asp Asp Gly Pro Asn Pro Val Val Pro
20 25 30

Ile Ala Tyr Lys Glu Glu Phe Arg Glu Thr Met Asp Tyr Phe Arg Ala
35 40 45

Ile Tyr Phe Ser Asp Glu Arg Ser Pro Arg Ala Leu Arg Leu Thr Glu
50 55 60

Glu Thr Leu Leu Leu Asn Ser Gly Asn Tyr Thr Val Trp His Phe Arg
65 70 75 80

Arg Leu Val Leu Glu Ala Leu Asn His Asp Leu Phe Glu Glu Leu Glu
85 90 95

Phe Ile Glu Arg Ile Ala Glu Asp Asn Ser Lys Asn Tyr Gln Leu Trp
100 105 110

His His Arg Arg Trp Val Ala Glu Lys Leu Gly Pro Asp Val Ala Gly
115 120 125

Arg Glu Leu Glu Phe Thr Arg Arg Val Leu Ser Leu Asp Ala Lys His
130 135 140

Tyr His Ala Trp Ser His Arg Gln Trp Thr Leu Arg Ala Leu Gly Gly
145 150 155 160

Trp Glu Asp Glu Leu Asp Tyr Cys His Glu Leu Leu Glu Ala Asp Val
165 170 175

Phe Asn Asn Ser Ala Trp Asn Gln Arg Tyr Tyr Val Ile Thr Gln Ser
180 185 190

Pro Leu Leu Gly Gly Leu Glu Ala Met Arg Glu Ser Glu Val Ser Tyr
195 200 205

Thr Ile Lys Ala Ile Leu Thr Asn Pro Ala Asn Glu Ser Ser Trp Arg
210 215 220

Tyr Leu Lys Ala Leu Tyr Lys Asp Asp Lys Glu Ser Trp Ile Ser Asp
225 230 235 240

Pro Ser Val Ser Ser Val Cys Leu Asn Val Leu Ser Arg Thr Asp Cys
245 250 255

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Phe His Gly Phe Ala Leu Ser Thr Leu Leu Asp Leu Leu Cys Asp Gly
 260 265 270
 Leu Arg Pro Thr Asn Glu His Lys Asp Ser Val Arg Ala Leu Ala Asn
 275 280 285
 Glu Glu Pro Glu Thr Asn Leu Ala Asn Leu Val Cys Thr Ile Leu Gly
 290 295 300
 Arg Val Asp Pro Ile Arg Ala Asn Tyr Trp Ala Trp Arg Lys Ser Lys
 305 310 315 320
 Ile Thr Val Ala Ala Ile
 325

<210> 21
 <211> 470
 <212> PRT
 <213> Lycopersicon esculentum

<400> 21
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 20 25 30
 Asn Ser Pro Ser Asp Leu Ile Glu Ile Glu Arg Asp Lys His Phe Gly
 35 40 45
 Tyr Leu Ser Gln Gly Leu Arg Lys Leu Gly Pro Ser Phe Ser Val Leu
 50 55 60
 Asp Ala Ser Arg Pro Trp Leu Cys Tyr Trp Thr Leu His Ser Ile Ala
 65 70 75 80
 Leu Leu Gly Glu Ser Ile Gly Gly Lys Leu Glu Asn Asp Ala Ile Asp
 85 90 95
 Phe Leu Thr Arg Cys Gln Asp Lys Asp Gly Gly Tyr Gly Gly Gly Pro
 100 105 110
 Gly Gln Met Pro His Leu Ala Thr Thr Tyr Ala Ala Val Asn Ser Leu
 115 120 125
 Ile Thr Leu Gly Lys Pro Glu Ala Leu Ser Ser Ile Asn Arg Glu Lys
 130 135 140
 Leu Tyr Thr Phe Leu Leu Arg Met Lys Asp Ala Ser Gly Gly Phe Arg
 145 150 155 160
 Met His Asp Gly Gly Glu Val Asp Val Arg Ala Cys Tyr Thr Ala Ile
 165 170 175
 Ser Val Ala Asn Ile Leu Asn Ile Val Asp Asp Glu Leu Ile His Gly
 180 185 190
 Val Gly Asn Tyr Ile Leu Ser Cys Gln Thr Tyr Glu Gly Gly Ile Ala
 195 200 205

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[illegible]

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<210> 22
<211> 419
<212> PRT
<213> Pisum sativum
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		35					40					45			
Cys	Tyr	Trp	Ile	Ile	His	Ser	Ile	Ala	Leu	Leu	Gly	Glu	Ser	Ile	Asp
	50					55					60				
Asp	Asp	Leu	Glu	Asp	Asn	Thr	Val	Asp	Phe	Leu	Asn	Arg	Cys	Gln	Asp
65					70					75					80
Pro	Asn	Gly	Gly	Tyr	Ala	Gly	Gly	Pro	Gly	Gln	Met	Pro	His	Leu	Ala
				85					90					95	
Thr	Thr	Tyr	Ala	Ala	Val	Asn	Thr	Leu	Ile	Thr	Leu	Gly	Gly	Glu	Lys
			100					105					110		
Ser	Leu	Ala	Ser	Ile	Asn	Arg	Asn	Lys	Leu	Tyr	Gly	Phe	Met	Arg	Arg
		115					120					125			
Met	Lys	Gln	Pro	Asn	Gly	Gly	Phe	Arg	Met	His	Asp	Glu	Gly	Glu	Ile
	130					135					140				
Asp	Val	Arg	Ala	Cys	Tyr	Thr	Ala	Ile	Ser	Val	Ala	Ser	Val	Leu	Asn
145					150					155					160
Ile	Leu	Asp	Asp	Glu	Leu	Ile	Lys	Asn	Val	Gly	Asp	Phe	Ile	Leu	Ser
				165				170						175	
Cys	Gln	Thr	Tyr	Glu	Gly	Gly	Leu	Ala	Gly	Glu	Pro	Gly	Ser	Glu	Ala
			180					185					190		
His	Gly	Gly	Tyr	Thr	Phe	Cys	Gly	Leu	Ala	Ala	Met	Ile	Leu	Ile	Gly
		195					200					205			
Glu	Val	Asn	Arg	Leu	Asp	Leu	Pro	Arg	Leu	Leu	Asp	Trp	Val	Val	Phe
		210				215					220				
Arg	Gln	Gly	Lys	Glu	Cys	Gly	Phe	Gln	Gly	Arg	Thr	Asn	Lys	Leu	Val
225					230					235					240
Asp	Gly	Cys	Tyr	Ser	Phe	Trp	Gln	Gly	Gly	Ala	Val	Ala	Leu	Leu	Gln
				245					250					255	
Arg	Leu	His	Ser	Ile	Ile	Asp	Glu	Gln	Met	Ala	Glu	Ala	Ser	Gln	Phe
			260					265					270		
Val	Thr	Val	Ser	Asp	Ala	Pro	Glu	Glu	Lys	Glu	Cys	Leu	Asp	Gly	Thr
		275					280					285			
Ser	Ser	His	Ala	Thr	Ser	His	Ile	Arg	His	Glu	Gly	Met	Asn	Glu	Ser
	290					295					300				
Cys	Ser	Ser	Asp	Val	Lys	Asn	Ile	Gly	Tyr	Asn	Phe	Ile	Ser	Glu	Trp
305					310					315					320
Arg	Gln	Ser	Glu	Pro	Leu	Phe	His	Ser	Ile	Ala	Leu	Gln	Gln	Tyr	Ile
				325					330					335	
Leu	Leu	Cys	Ser	Gln	Glu	Gln	Asp	Gly	Gly	Leu	Arg	Asp	Lys	Pro	Gly
			340					345					350		

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<400> 23															
Met	Glu	Ala	Ser	Thr	Ala	Ala	Glu	Thr	Pro	Thr	Pro	Thr	Val	Ser	Gln
1				5					10					15	
Arg	Asp	Gln	Trp	Ile	Val	Glu	Ser	Gln	Val	Phe	His	Ile	Tyr	Gln	Leu
			20					25					30		
Phe	Ala	Asn	Ile	Pro	Pro	Asn	Ala	Gln	Ser	Ile	Ile	Arg	Pro	Trp	Leu
		35					40					45			
Cys	Tyr	Trp	Ile	Ile	His	Ser	Ile	Ala	Leu	Leu	Gly	Glu	Ser	Ile	Asp
	50					55					60				
Asp	Asp	Leu	Glu	Asp	Asn	Thr	Val	Asp	Phe	Leu	Asn	Arg	Cys	Gln	Asp
65					70					75					80
Pro	Asn	Gly	Gly	Tyr	Ala	Gly	Gly	Pro	Gly	Gln	Met	Pro	His	Leu	Ala
				85					90					95	
Thr	Thr	Tyr	Ala	Ala	Val	Asn	Thr	Leu	Ile	Thr	Leu	Gly	Gly	Glu	Lys
			100					105					110		
Ser	Leu	Ala	Ser	Ile	Asn	Arg	Asn	Lys	Leu	Tyr	Gly	Phe	Met	Arg	Arg
		115					120					125			
Met	Lys	Gln	Pro	Asn	Gly	Gly	Phe	Arg	Met	His	Asp	Glu	Gly	Glu	Ile
	130					135					140				
Asp	Val	Arg	Ala	Cys	Tyr	Thr	Ala	Ile	Ser	Val	Ala	Ser	Val	Leu	Asn
145					150					155					160
Ile	Leu	Asp	Asp	Glu	Leu	Ile	Lys	Asn	Val	Gly	Asp	Phe	Ile	Leu	Ser
				165					170					175	
Cys	Gln	Thr	Tyr	Glu	Gly	Gly	Leu	Ala	Gly	Glu	Pro	Gly	Ser	Glu	Ala
			180					185					190		
His	Gly	Gly	Tyr	Thr	Phe	Cys	Gly	Leu	Ala	Ala	Met	Ile	Leu	Ile	Gly
		195					200					205			

Glu	Val	Asn	Arg	Leu	Asp	Leu	Pro	Arg	Leu	Leu	Asp	Trp	Val	Val	Phe	210	215	220
Arg	Gln	Gly	Lys	Glu	Cys	Gly	Phe	Gln	Gly	Arg	Thr	Asn	Lys	Leu	Val	225	230	235
Asp	Gly	Cys	Tyr	Ser	Phe	Trp	Gln	Gly	Gly	Ala	Val	Ala	Leu	Leu	Gln	245	250	255
Arg	Leu	His	Ser	Ile	Ile	Asp	Glu	Gln	Met	Ala	Glu	Ala	Ser	Gln	Phe	260	265	270
Val	Thr	Val	Ser	Asp	Ala	Pro	Glu	Glu	Lys	Glu	Cys	Leu	Asp	Gly	Thr	275	280	285
Ser	Ser	His	Ala	Thr	Ser	His	Ile	Arg	His	Glu	Gly	Met	Asn	Glu	Ser	290	295	300
Cys	Ser	Ser	Asp	Val	Lys	Asn	Ile	Gly	Tyr	Asn	Phe	Ile	Ser	Glu	Trp	305	310	315
Arg	Gln	Ser	Glu	Pro	Leu	Phe	His	Ser	Ile	Ala	Leu	Gln	Gln	Tyr	Ile	325	330	335
Leu	Leu	Cys	Ser	Gln	Glu	Gln	Asp	Gly	Gly	Leu	Arg	Asp	Lys	Pro	Gly	340	345	350
Lys	Arg	Arg	Asp	His	Tyr	His	Ser	Cys	Tyr	Cys	Leu	Ser	Gly	Leu	Ser	355	360	365
Leu	Cys	Gln	Tyr	Ser	Trp	Ser	Lys	Arg	Pro	Asp	Ser	Pro	Pro	Leu	Pro	370	375	380
Lys	Val	Val	Met	Gly	Pro	Tyr	Ser	Asn	Leu	Leu	Glu	Pro	Ile	His	Pro	385	390	395
Leu	Phe	Asn	Val	Val	Leu	Asp	Arg	Tyr	Arg	Glu	Ala	His	Glu	Phe	Phe	405	410	415
Ser	Gln	Leu																

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